

# FIG. 1

BLASTP - query = 147\_TR1; Hit = swiss|O15393|TMS2\_HUMAN

This hit is scoring at : 3e-66 (expectation value)

Alignment length (overlap) : 370

Identities : 38 %

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Database searched : nrdb

Q: 36 CDGVVDCKLKSDDELGCVRFWDKSLKLIYSGSSHQWLPICSSNWNDYSEKTCQQLGFES  
 CDGV .C. .DE CVR. . . :L::YS.....W P:C...WN::Y....C::G:::  
 H: 133 CDGVSHCPGGEDENRCVRLYGPNFILQMYSSQRKSWHPVCQDDWNENYGRAACRDMGYKN

AHRTTEVAHRDFANSFSILRYNST IQESLHRSE CPSQRYISLQCSHCGLRA  
 . : : . D : .S S : : .N : : I : .L : .S : C : S : : .SL : C CG : . : :  
 NFYSSQGIVDD SGSTSFMKLNTSAGNVDIYKKLYHSDACSSKAVVSLRCLACGVNLNSS

MTGRIVGGALASDSKWPWQVSLHFGTTHCGGTLIDAQWVLTAAHCFFVTREKVLEG---  
 ...RIVGG. A ...WPWQVSLH. ...H:CGG::I::W::TAAHC. EK L..  
 RQSRIVGGESALPGAWPWQVSLHVQNVHVCGGSIITPEWVTAACHV EKPLNNPWH  
 TRYPSIN HIS

WKVYAGTSNLHQLEAAS--IAEIIINSNYTDEEDDYDIALMRLSKETLSGEGICTP  
 W...AG. . . : .A. : : : I : .NY : : : : DIALM:L.KPLT... : :C.P  
 WTAFAFILRQSFMEFYGAGYQVQKVISHPNYDSKTKNNDIALMKLQKPLTFNDLVKPVCLP

RSPAPQPOHPLOPSHLSASVNSYPGPKASADKTSPLREVQVNLIDFKKENDYLIVYDSYL  
 . P LQP..L . : : : G : : : : KTS..L...V LI : : :CN. .VYD : : :  
 N PGMMLOPEQL-CWISGWGATEEKGKTSEVLNAAKVLLIETQRCNSRYVDNLI

TPRMMCAGDLRGGRDSCQGDGGPLVCEQNNRWYLAGVTSWGTGCGQRNKPVGYYTKVTEV  
 TP.M:CAG L:G. DSCQGDGGPLV...NN W:L:G TSWG:GC...:PGVY .V. .  
 TPAMICAGFLQGNVDSCQGDGGPLVTSNNNIWWLIGDTSWGSACAKAYRPGVYGNVMVF

TRYPSIN\_SER

LPWIYSKMEA 389

..WIY.:M:A

TDWIYRQMKA 490

## FIG. 2

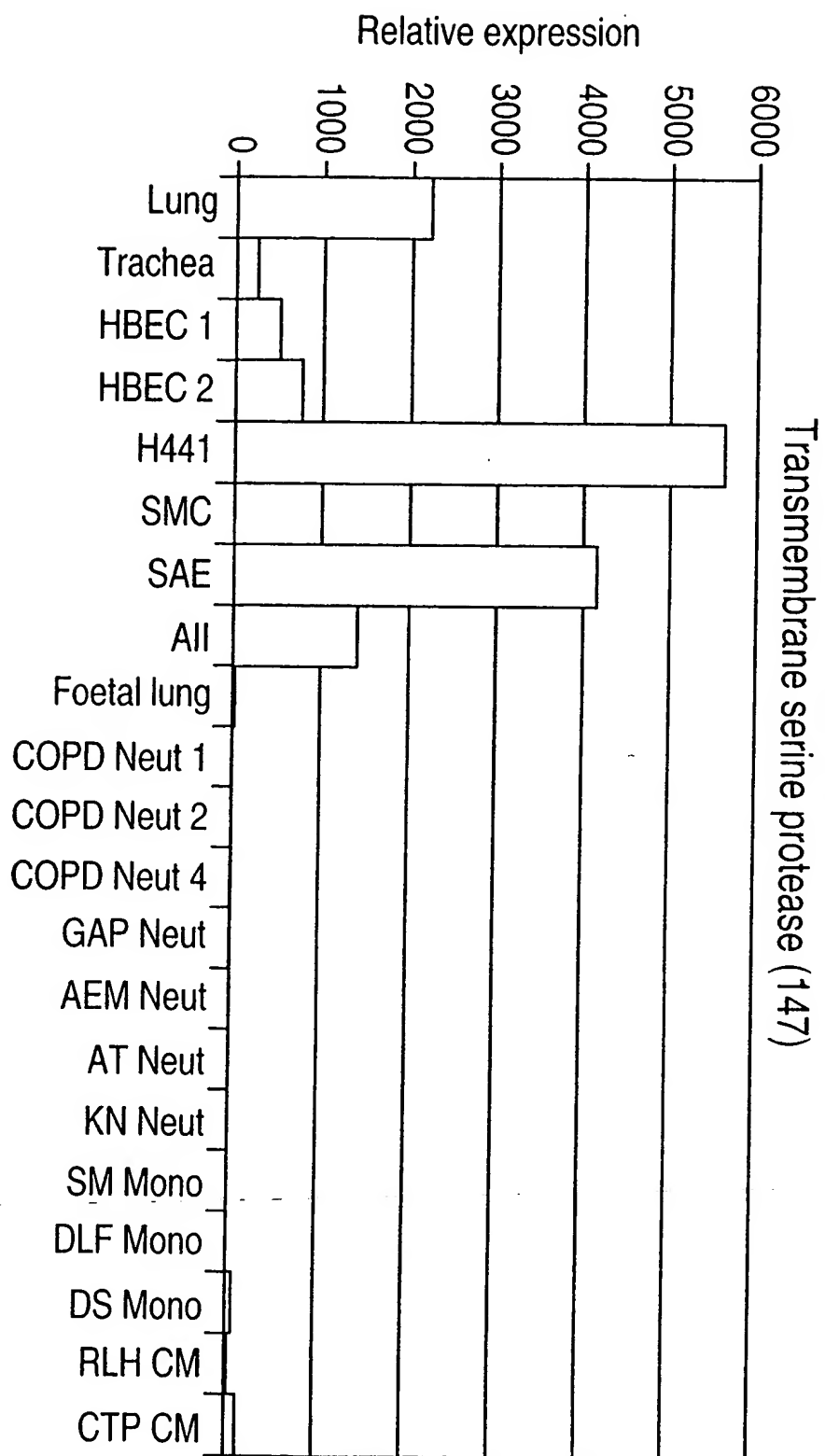
Prosite search results

PS00134	187->193 TRYPSIN_HIS	PDOC00124
PS00135	334->346 TRYPSIN_SER	PDOC00124

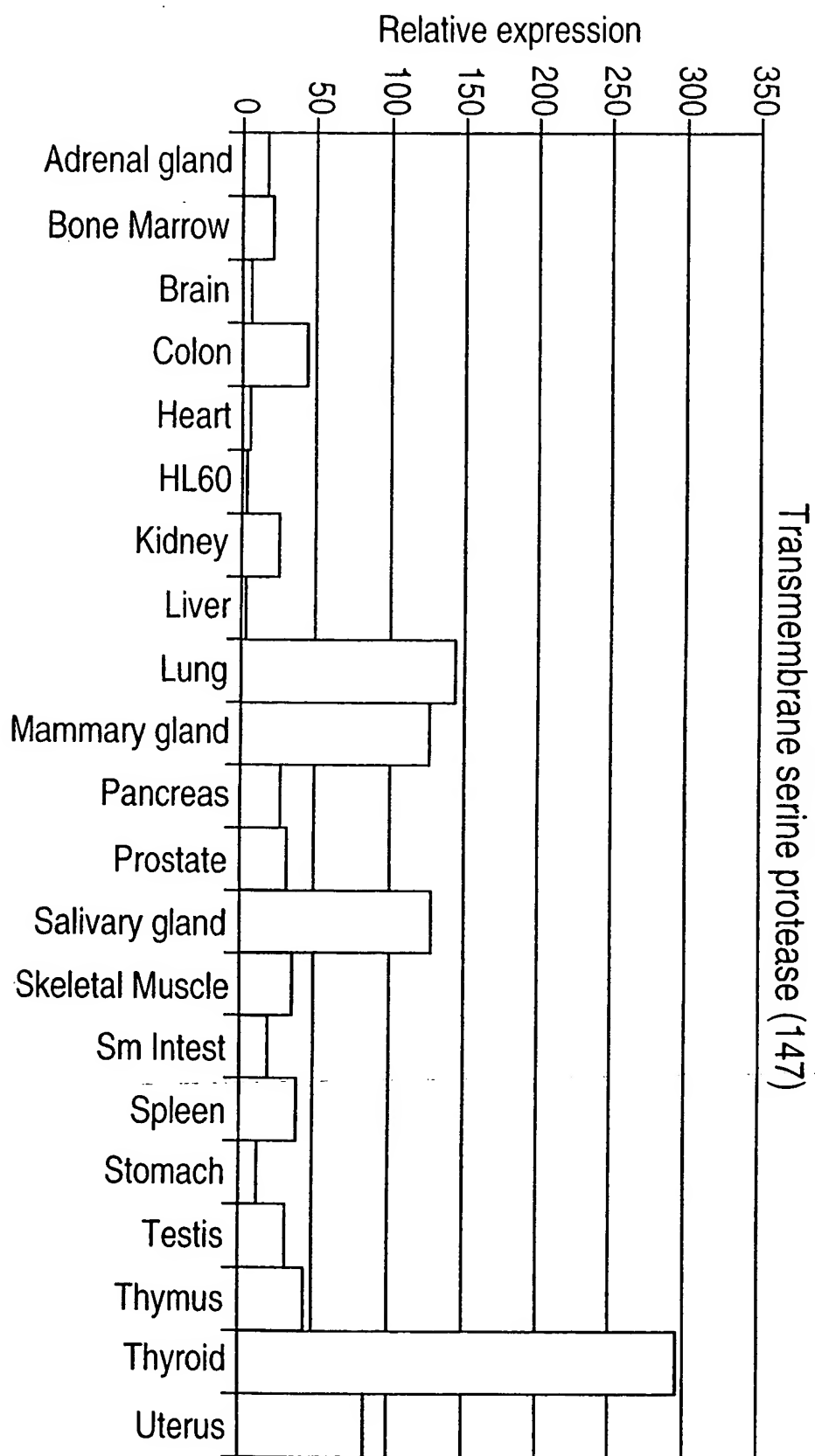
## FIG. 3

### BLOCKS search results

AC#	Description	Strength	Score
BL00495N AA#	Apple domain proteins. 325 AGdlrGGrDsCqGDSGGPLVCeqNnRWyLaGvTSW (SEQ ID NO:15)	1945	1582
BL01253G AA#	Type I fibronectin domain proteins. 332 rDsCQGDSGGPLVC (SEQ ID NO:16)	1641	1548
BL00134A AA#	Serine proteases, trypsin family, histidine p 175 CGGTLIDAQWVLTAHC (SEQ ID NO:17)	1500	1524
BL00021D AA#	Kringle domain proteins. 341 GPLVCEQNNRWYLaGVTSWGtGCGQRNKPGVYTKVTevLPWI (SEQ ID NO:18)	1556	1510
BL01253H AA#	Type I fibronectin domain proteins. 351 wYLaGvtSWGtGCGQRNKPGVYTKVTevLpWIysk (SEQ ID NO:19)	1765	1508
BL00021B AA#	Kringle domain proteins. 175 CGGTLIDaQWVLTAHCF (SEQ ID NO:20)	1547	1507
BL00495O AA#	Apple domain proteins. 360 GtGCGQRnkPGVYTKVTevlpWIysKmeA (SEQ ID NO:21)	1756	1383
BL00134B AA#	Serine proteases, trypsin family, histidine p 333 DSCQGDSGGPLVCEqNNRWYLAGV (SEQ ID NO:22)	1289	1299
BL01209 AA#	LDL-receptor class A (LDLRA) domain proteins. 35 CDGVVDCKlKSDE (SEQ ID NO:23)	1413	1274
BL01253F AA#	Type I fibronectin domain proteins. 288 AdktSpFLREvQVnLidfkKCndylVYdSylTPrMmCAG (SEQ ID NO:24)	1693	1270
BL00495L AA#	Apple domain proteins. 209 tSnlhqlpeaaSlaEIIInsNYtdeEddyDIALmrLskP (SEQ ID NO:25)	1947	1263
BL00134C AA#	Serine proteases, trypsin family, histidine p 369 PGVYTKVTEVLPWI (SEQ ID NO:26)	1245	1254
BL01253D AA#	Type I fibronectin domain proteins. 175 CGGtLIdaqWVLTA (SEQ ID NO:27)	1398	1217



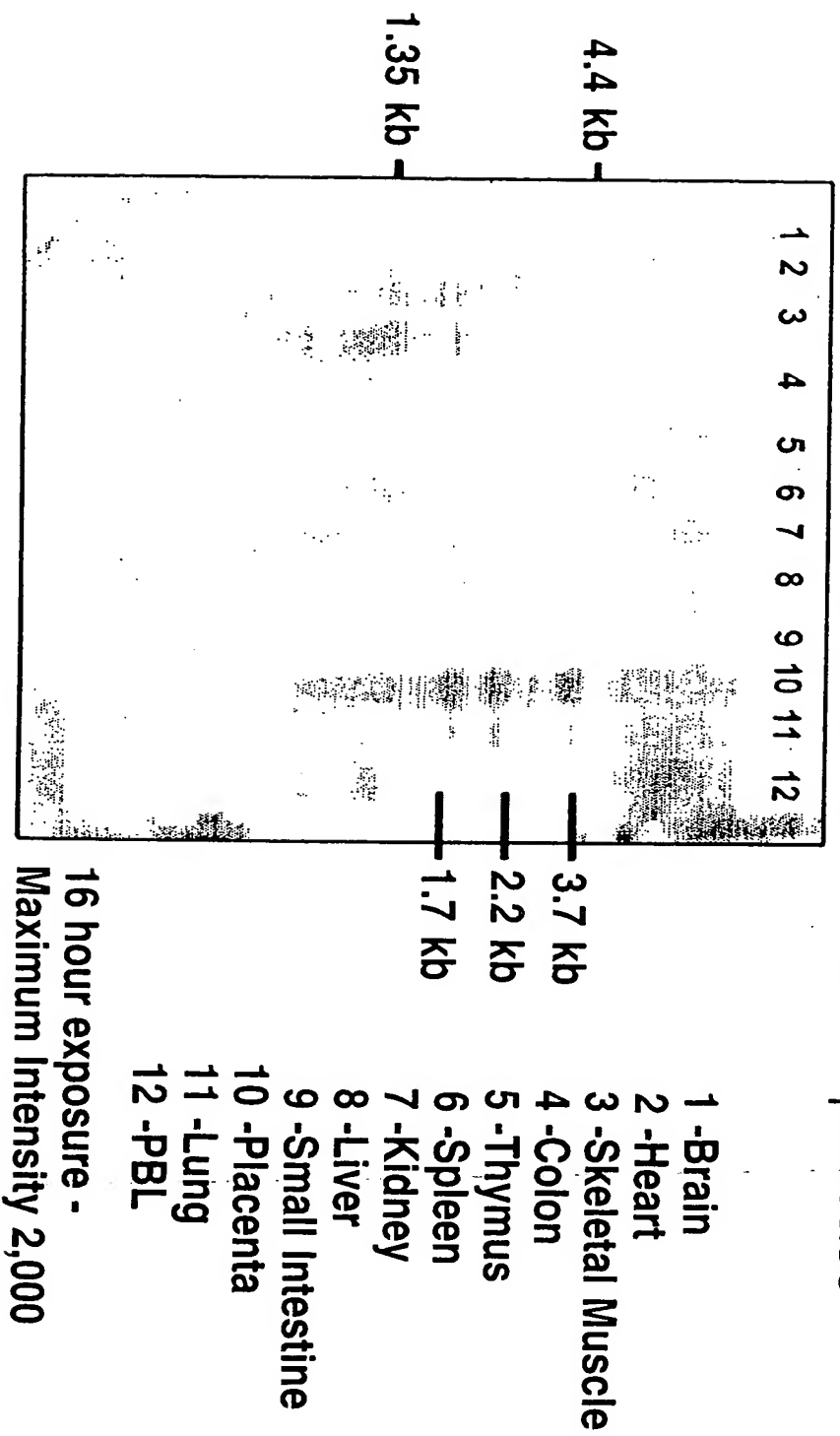
**FIG. 4**

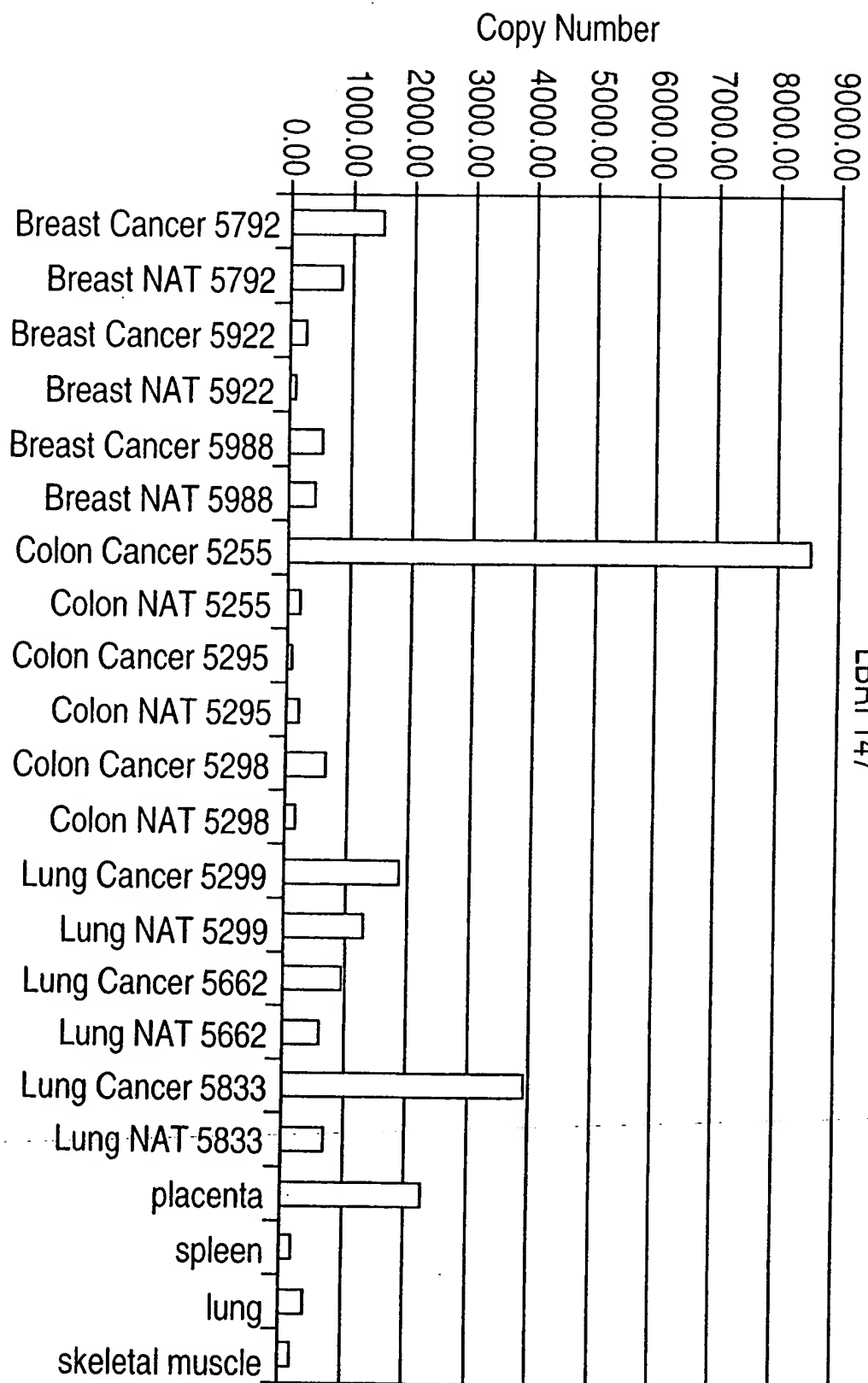


**FIG. 5**

**FIG. 6**

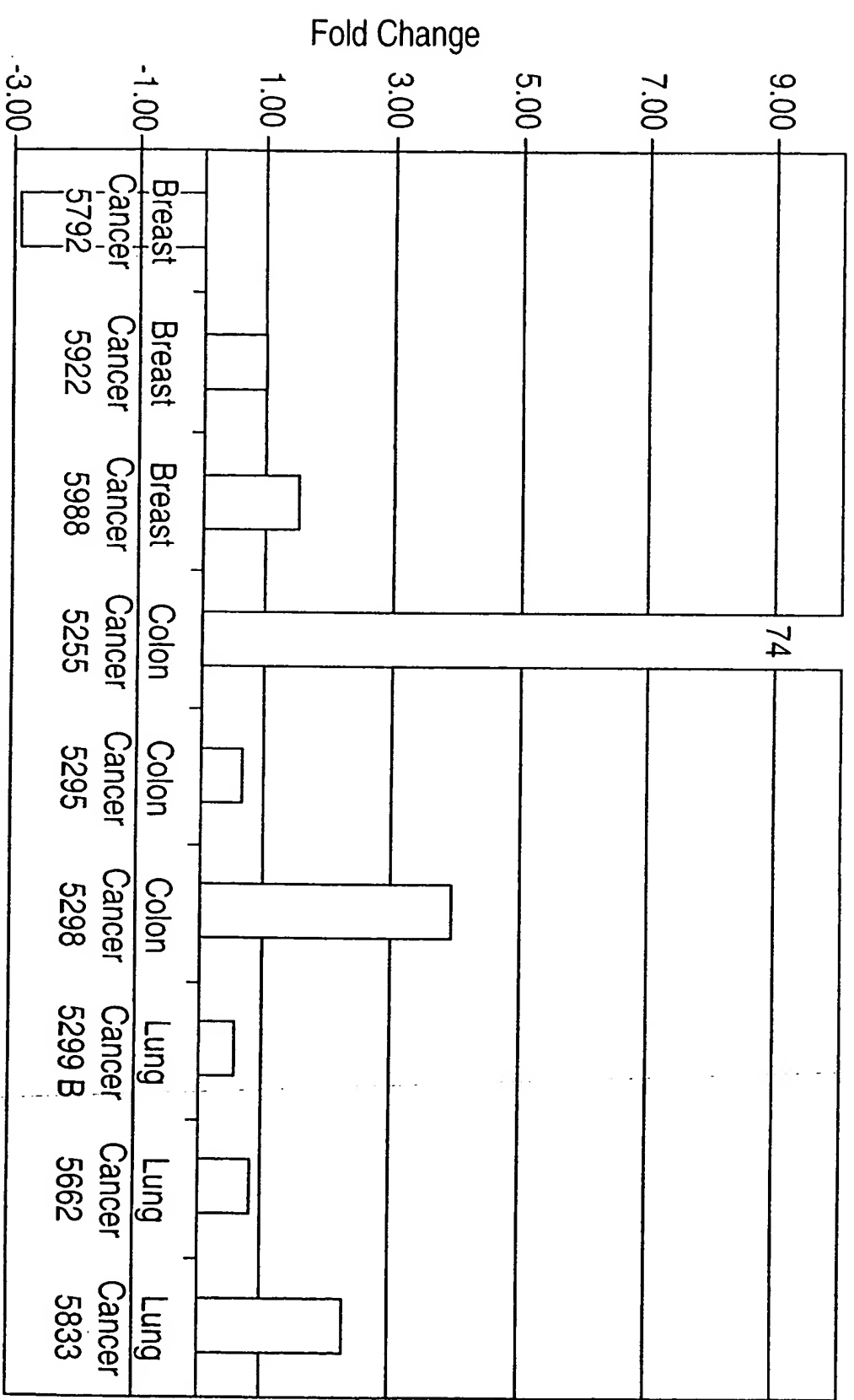
**LBRI -147 - Transmembrane serine protease**





**FIG. 7**  
LBRI 147

**FIG. 8**  
LBRI 147: Fold Change





**FIG. 9**

